Amendments to the Specification:

Please delete paragraphs 50, 51, and 79 in their entirety and enter the following replacement paragraphs as substitutes therefor:

[50] Labeling was performed at Incyte Genomics, Inc. (Fremont, CA). Two hundred nanograms of mRNA was reverse transcribed using cy3- or cy5-labeled fluorescent primers; appropriate matched control and schizophrenic sample pairs were combined, and hybridized onto the same UniGEM-V cDNA microarray. Each UniGEM-V array contained over 7,000 unique and sequence-verified cDNA elements mapped to 6,794 UniGene *Homo sapiens* annotated clusters found at the ~~following~~ NIH website: ~~"http://www.ncbi.nlm.nih.gov/UniGene/index.html"~~. Hybridization and washing was performed using proprietary Incyte protocols. If a gene or expressed sequence tag (EST) was differentially expressed, the cDNA feature on the array bound more of the labeled probe from one sample than the other, producing either a greater cy3 or cy5 signal intensity. The microarrays were scanned under cy3-cy5 dual fluorescence, and the resulting images were analyzed for signal intensity. If the cy3 vs. cy5 signal intensity was within three fold, and the microarray detected spiked-in control standard less abundant than 1 copy in 50,000, the raw data were exported to a local SQL server database. On the server, the data were further analyzed using GemTools (Incyte's proprietary software) and MS-Excel 2000. Note that the operators performing the labeling, hybridization, scanning, and signal analysis were blind to the specific category to which each sample belonged.

[51] A gene was considered to be expressed if the DNA sample was successfully amplified by PCR, produced signal from at least 40% of the spot surface, and had a signal/background ratio over 5-fold for either the cy3 or cy5 probe. Based on Incyte's control hybridization studies ~~"http://www.incyte.com/reagents/gem/products.shtml/GEM-reproducibility.pdf")~~ and control experiments, array data reliability and reproducibility cutoffs were established as follows:

[79] A panel of 10 African-American cases and 6 Caucasian controls was initially used to screen for polymorphisms in the exonic, intronic, and flanking genomic sequences of the RGS4 gene. The re-sequenced region included 6.8 kb upstream and 2.9 kb downstream of the coding sequence. The genomic sequence was used to design primers and amplicons ~500bp were generated, with overlapping sequences. The amplified fragments were sequenced using an ABI 3700 DNA sequencer. The sequencing panel that was used (n = 16) has over 80% power to detect SNPs with minor allele frequency over 5% (Kruglyak *et al. Nature Gen.* **27**, 234-236, 2001, which is hereby incorporated by reference). We also sequenced cDNA sequences from the post-mortem samples reported on earlier (Mirnics *et al. Mol. Psychiatry* **6**, 293-301, 2001). The sequences were aligned using Sequencher (version 4.5) and polymorphisms were numbered consecutively. Additional SNPs localized to NT_022030 were obtained from the NCBI SNP database ~~("http://www.ncbi.nlm.nih.gov/SNP")~~. We also obtained genotype data from a prior study of the NIMH sample ~~("http://zork.wustl.edu/nimh"~~.